



1

SEQUENCE LISTING

101725, 284

<110> ADLER, JON ELLIOT
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY

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<140> 10/035,045

<141> 2002-01-03

<150> 60/259,227

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<212> DNA

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 <212> PRT
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Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
          35             40             45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
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Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
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Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	
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Thr	Ser	Asp	Leu	Val	Met	Gly	Leu	Pro	Gly	Met	Ala	Gln	Met	Gly	Thr	
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Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Gln	Leu	His	Glu	Phe	Pro	Gln	
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Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser	
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 465 470 475 480
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 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
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 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
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 755 760 765
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 770 775 780
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 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
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 <212> DNA
 <213> Artificial Sequence

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<210> 7
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 <212> PRT
 <213> Homo sapiens

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<210> 8
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 <213> Homo sapiens

<400> 8

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<210> 9

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<212> DNA

<213> Mus sp.

<400> 9

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Ala Ser Gly Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
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Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser
          50           55           60
Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
          65           70           75           80
Ser Thr Leu Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu
          85           90           95
Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Asp Ser Gly
          100          105          110
Leu Leu Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala
          115          120          125
Trp Tyr Leu Thr Ala Ser Pro Glu Val Val Thr Asp Trp Ser Val Leu
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Pro Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Asn Leu
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<211> 2526

<212> DNA

<213> Homo sapiens

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<211> 841

<212> PRT

<213> Homo sapiens

<400> 17

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 35 40 45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
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Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
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Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
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Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
 100 105 110

Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
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 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
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 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
 275 280 285
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 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
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 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
 325 330 335
 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
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 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Consensus sequence

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<222> (1)

<223> Thr or Arg

<220>

<221> MOD RES

<222> (3)

<223> Phe or Leu

<220>

<221> MOD RES

<222> (4)

<223> Arg, Gln or Pro

<220>

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<222> (6)

<223> Arg or Thr

<220>

<221> MOD RES

<222> (7)

<223> Ser, Pro or Val

<220>
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 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

<220>
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 <222> (11)
 <223> Ala or Glu

<220>
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 <223> Trp or Leu

<220>
 <221> MOD_RES
 <222> (13)
 <223> Arg, His or Gly

<400> 18
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
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<210> 19
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
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 <223> Leu or Gln

<220>
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 <223> Glu, Gly or Thr

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 <223> Asn, Arg or Cys

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 <223> Arg or Glu

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<223> Arg or Lys

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<221> MOD_RES

<222> (10)

<223> Cys, Gly or Phe

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<221> MOD_RES

<222> (11)

<223> Val, Leu or Ile

<220>

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<223> Phe or Leu

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<222> (14)

<223> Ala or Ser

<220>

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<222> (15)

<223> Met or Leu

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<211> 3563

<212> DNA

<213> Homo sapiens

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<210> 21

<211> 839

<212> PRT

<213> Homo sapiens

<400> 21

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Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
    35                      40                      45

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Tyr	Phe	Leu	Ala	His	Glu	Asp	Asn	Leu	Leu	Pro	Ile	Gln	Glu	Asp	Tyr
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Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu
225					230					235					240
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg
				245					250					255	
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val
			260					265					270		
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val
		275					280					285			
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		290				295					300				
Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	Gly	His	Leu	Gly
305					310					315					320
Thr	Phe	Leu	Gly	Ile	Thr	Ile	Gln	Ser	Val	Pro	Ile	Pro	Gly	Phe	Ser
				325					330					335	
Glu	Phe	Arg	Glu	Trp	Gly	Pro	Gln	Ala	Gly	Pro	Pro	Pro	Leu	Ser	Arg
			340					345					350		

Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
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 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
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 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620
 Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
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 Gly Tyr Thr Met Arg Arg Asp
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 PDZIP peptide sequence

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 <211> 2520
 <212> DNA
 <213> Homo sapiens

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gagtatgaag tgaaggtgat aggetacaac ctcatgcagg ccatgcgctt cgcggtggag 240
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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Six-His tag

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His His His His His His

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5